

## LISTING OF CLAIMS

1. (Currently Amended) An assay for assessing the risk of cancer in a healthy individual, wherein said assay comprises the steps of;

- (i) isolating a population of cells from normal tissue of said individual, and
  - (ii) quantitatively determining the frequency of epimutation present in a tumor suppressor gene in said population of cells, and
  - (iii) assessing said risk based on said frequency of epimutation present in a tumor suppressor,
- wherein (A) the epimutation of said tumor suppressor gene is associated with said cancer, (B) the epimutation is DNA methylation, and (C) said tumor suppressor gene is other than one that is subject to normal parent of origin-specific expression, **and (D) wherein said cancer is selected from the group consisting of breast cancer, ovarian cancer, malignant melanoma, pancreatic cancer, prostate cancer, retinoblastoma, leukemia, lymphoma, renal cancer, endometrial cancer, paraganglioma, pheochromocytoma, basal cell carcinoma, soft tissue carcinoma, brain tumors, testicular cancers, and gynecological malignancies.**

2. (Currently Amended) The assay of claim 1, wherein the normal tissue is selected from the group consisting of ~~normal peripheral blood~~, normal hair follicle tissue and normal tissue from the buccal cavity.

3. (Original) The assay of claim 1, wherein the normal tissue is normal peripheral blood.

4. (Canceled)

5. (Previously Presented) The assay of claim 1, wherein the epimutation is present in the promoter or other regulatory region of the gene and is associated with transcriptional silencing of said gene.

6-7. (Canceled)

8. (Previously Presented) The assay of claim 1, wherein the epimutation is present in a gene selected from the group consisting of *hMLH1*, *hMSH2*, *APC1A*, *APC1B* and *p16*.

9. (Original) The assay of claim 8, wherein the epimutation is present in *hMLH1*.